Emerging baselines to estimate migration patterns of Dolly Varden charr in nearshore waters and the high-seas

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Introduction

Dolly Varden is a dominant freshwater species in arctic and subarctic eastern Russia, Alaska, and western Canada and an important food source for indigenous peope in these regions.

Anadromous Dolly Varden are distributed throughout Alaska and occupy a wide variety of habitats, from coastal streams in the southeast panhandle to rivers draining the North

Slope. Anadromous Dolly Varden show highly complex migration patterns. They typically feed in marine waters in the summer, home to spawn in their natal streams, and overwinter in natal and non-natal freshwater lakes and rivers in mixed aggregates. Two subspecies of Dolly Varden have been described in North America, and they appear to differ greatly in their marine migrations. Southern form Dolly Varden typically do not migrate far from natal and overwintering streams, while long distance migrations exceeding 1,600 km have been documented for northern form Dolly Varden (Bernard et al. 1992; DeCicco 1992). Differences in migration patterns may be due to frequency of spawning and other life history differences.

Migration patterns have typically been evaluated using tagging and radio telemetry studies. Our objectives are to:
1) use microsatellite and mitochondrial DNA markers to estimate population structure in Alaska and
2) use mixed-stock analysis (MSA) to identify the origin of Dolly Varden sampled from overwintering areas, coastal catches, and offshore samples to evaluate population specific migration patterns.

Methods

Sampling locations in Alaska:

Dolly Varden have been sampled at 37 locations in Alaska. Only prespawning Dolly Varden on the spawning grounds or juvenile Dolly Varden were sampled to ensure collections did not comprise overwintering groups from multiple tributaries.

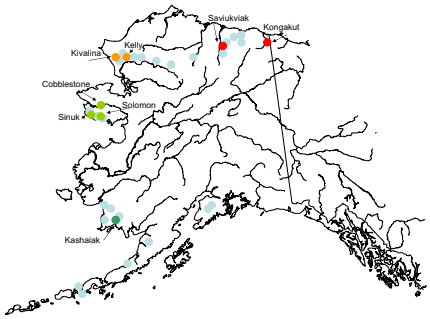
Genetic Markers:

Genetic variation is assayed at seven microsatellite loci we developed: *Sma-3*,-5*, -10*, -17*, -21*, -22*,* and *-24**.

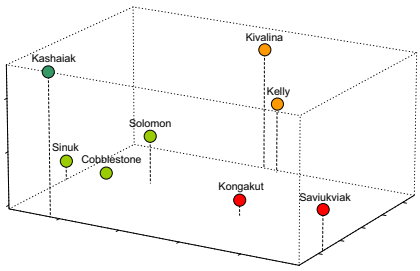
Mitochondrial DNA (mtDNA) variation is assayed in three segments of the mtDNA genome (cytochrome b, ND1/2, and ND5/6) using 14 enzymes in a subset of 20 populations.

The results presented focus on eight populations of northern form Dolly Varden assayed for variation at both marker types:

North Slope: Kongakut, Saviukviak R.
Kotzebue Sound: Kivalina, Kelly R.
Norton Sound: Cobblestone, Sinuk
Solomon R.,
Togiak River: Kashaiak R.



Results



Objective1: Population structure of Dolly Varden in Alaska:

Northern form:
•Microsatellite loci are highly polymorphic: H_O=0.684, average number of alleles per locus=19.7.

•Significant allele frequency differences detected among all population pairs.

•14 mtDNA haplotypes observed; haplotype diversity=0.523, nucleotide diversity=0.002

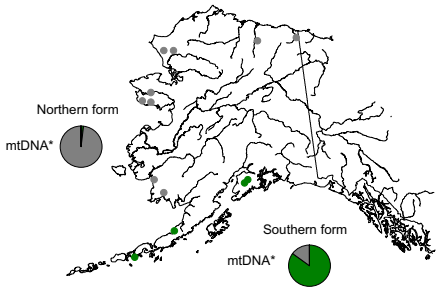
•Multidimensional scaling of distances calculated from microsatellite data indicates genetic relationships follow geographic proximity and life history variation:

Northern form Dolly Varden in Norton Sound drainages south to the Alaska Peninsula are smaller than those found in Kotzebue Sound and Beaufort Sea drainages, and their movement patterns for feeding follow the movements of Pacific salmon (DeCicco and Reist 1999).

Northern and southern form:
•Differences in haplotype frequencies are observed between northern form and southern form Dolly Varden.

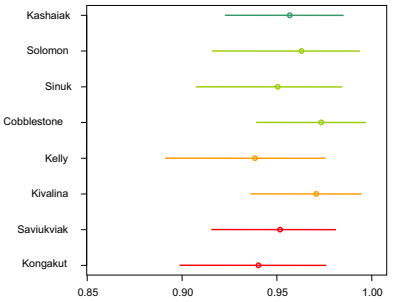
The common haplotype in southern form Dolly Varden has only been detected in a few individuals north of the Alaska Peninsula.

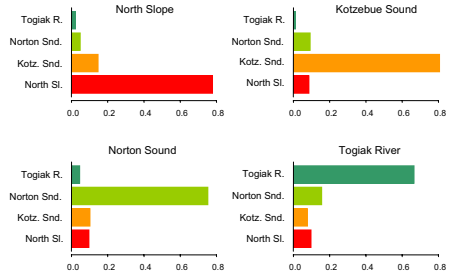
Mitochondrial data collected in this study can be merged with an mtDNA survey for Asian Dolly Varden (Oleynik et al. In press)



Objective 2: Identify the origin of Dolly Varden sampled from mixtures

Simulation analyses were conducted in SPAM ver 3.7 to test whether allele frequency differences among collections are large enough for MSA. Rare alleles were pooled and a Bayesian estimator of baseline allele frequencies was used to account for sampling error. Conditional maximum likelihood estimates of population contributions were made for 1000 artificial mixes (n=400) from a single population so that mean contribution estimates should equal 100%.
•Mean contribution estimates exceeded 90% for all populations.





Individual assignment tests were conducted using the direct classification method in Geneclass because the incidence of Dolly Varden in coastal waters is likely to be low.
•Percent of individuals classified to the correct region was approximately 80% for individuals from the North Slope, Kotzebue Sound, and Norton Sound, and 70% for Togiak River.

Conclusion

Microsatellite and mtDNA data show promise in identifying the origin of Dolly Varden sampled from overwintering areas as well as coastal and offshore waters.

Literature cited

Bernard DR, Hepler KR, Jones DJ, Whalen ME, McBride DN (1995) *Trans. Am. Fish. Soc.* ***124***, 297-307.
DeCicco AL, Reist RJ (1999) *ISACF Information Series* No. ***7***,13-19.
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